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Response Under 37 C.F.R. 1.116 - Expedited Procedure
Examining Group 1642

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By: _____ Printed: Diane Kizer

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

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In re Application of: Hillman et al.

Title: TUMORIGENESIS PROTEIN

Serial No.:	09/848,915	Filing Date:	May 04, 2001
Examiner:	Huff, S.	Group Art Unit:	1642

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BRIEF ON APPEAL

Sir:

Further to the Notice of Appeal filed June 30, 2003, and received by the USPTO on July 3, 2003, and in consideration of the Advisory Action mailed July 14, 2003, herewith are three copies of Appellants' Brief on Appeal. Appellants hereby request a one-month extension of time in order to file this Brief. Authorized fees include the statutory fee of $110.00 for a one-month extension of time, as well as the $ **330.00** fee for the filing of this Brief.

This is an appeal from the decision of the Examiner finally rejecting Claims 1-2 and 15-16 of the above-identified application.

(1) REAL PARTY IN INTEREST

The above-identified application is assigned of record to Incyte Pharmaceuticals, Inc. (now Incyte Corporation, formerly known as Incyte Genomics, Inc.) (Reel 9152, Frame 0605), which is the real party in interest herein.

(2) RELATED APPEALS AND INTERFERENCES

Appellants, their legal representative and the assignee are not aware of any related appeals or interferences which will directly affect or be directly affected by or have a bearing on the Board's decision in the instant appeal.

(3) STATUS OF THE CLAIMS

Claims rejected:	Claims 1-2 and 15-16
Claims allowed:	(none)
Claims canceled:	Claims 7, 17, 19-43
Claims withdrawn:	Claims 3-6, 8-14, 18, and 44-46[1]
Claims on Appeal:	Claims 1-2 and 15-16 (A copy of the claims on appeal, as amended, can be found in the attached Appendix.)

(4) STATUS OF AMENDMENTS AFTER FINAL

There were no amendments submitted after Final Rejection.

(5) SUMMARY OF THE INVENTION

Appellants' invention is directed, *inter alia*, to a polypeptide ("HTAP") having strong homology to murine lymphomagenesis-associated protein, BUP (GI 265569), and compositions containing it. This invention has a variety of utilities, e.g., in expression profiling, and in particular for diagnosis of conditions or diseases characterized by expression of HTAP, for toxicology testing, and for drug discovery. (See the Specification at, e.g., page 33, lines 8-16 and page 37, line 18 through page 38, line 6.). As described in the Specification:

> In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:1, as shown in Figures 1A and 1B. HTAP is 195 amino acids in length and has three potential casein kinase II phosphorylation sites encompassing residues S35-D38, T85-E88, and S162-E165, and one potential protein kinase C phosphorylation site encompassing residues S129-R131. HTAP has chemical and structural homology with a murine lymphomagenesis-associated protein, BUP (GI 265569; SEQ ID NO:3). In

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[1]The Advisory Action mailed July 14, 2003, does not list Claim 46 as a withdrawn claim. Appellants assume this omission of Claim 46 from the withdrawn claims was inadvertent.

particular, HTAP and BUP share 89% identity. As illustrated by Figures 3A and 3B, HTAP and BUP have rather similar hydrophobicity plots. Northern analysis shows the expression of this sequence in various cDNA libraries, at least 58% of which are immortalized or cancerous, 14% of which are associated with inflammation, and 14% associated with normal growth and development occurring in tissues of a fetus or child. (Specification, page 11, lines 7-17.)

(6) ISSUES

1. Whether the polypeptide variants and fragments of Claims 1 and 15 meet the written description requirement of 35 U.S.C. §112, first paragraph.

2. Whether Claims 1-2 and 15-16 directed to a polypeptide ("HTAP") having strong homology to murine lymphomagenesis-associated protein, BUP (GI 265569) meet the utility requirement of 35 U.S.C. §101.

3. Whether one of ordinary skill in the art would know how to use the claimed polypeptide, e.g., in toxicology testing, drug development, and the diagnosis of disease, so as to satisfy the enablement requirement of 35 U.S.C. §112, first paragraph.

(7) GROUPING OF THE CLAIMS

As to Issue 1

This issue pertains only to Claim 1 and 15.

As to Issue 2

All of the claims on appeal are grouped together and thus stand or fall together.

As to Issue 3

All of the claims on appeal are grouped together and thus stand or fall together.

(8) APPELLANTS' ARGUMENTS

Issue 1 Written Description Rejection

The Examiner rejected Claims 1 and 15 under 35 U.S.C. § 112, first paragraph, alleging that the claimed polypeptide variants and fragments and compositions comprising polypeptide

variants and fragments were not adequately described. In particular, the Examiner alleged that "a polypeptide having at least 90-99% sequence identity to SEQ ID NO:1" and the claimed polypeptide fragments are not adequately described. (Office Action mailed October 29, 2002, pages 4-5.)

In the Final Office Action, the Examiner ignores the claim limitations of "a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1" and "an immunogenic fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1" and attempts to introduce a limitation of biological "function" to the polypeptide variants and fragments, a limitations which is not present in the rejected claims. The Examiner ignores the limitation that the claimed polypeptides comprise a naturally-occurring amino acid sequence or is a fragment of a naturally-occurring amino acid sequence. (Office Action mailed October 29, 2002, pages 4-5 and Final Office Action, pages 2-3.)

The requirements necessary to fulfill the written description requirement of 35 U.S.C. 112, first paragraph, are well established by case law.

> . . . the applicant must also convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the "written description" inquiry, *whatever is now claimed. Vas-Cath, Inc. v. Mahurkar*, 19 USPQ2d 1111, 1117 (Fed. Cir. 1991)

Attention is also drawn to the Patent and Trademark Office's own "Guidelines for Examination of Patent Applications Under the 35 U.S.C. Sec. 112, para. 1", published January 5, 2001, which provide that :

> An applicant may also show that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics which provide evidence that applicant was in possession of the claimed invention, i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics. What is conventional or well known to one of ordinary skill in the art need not be disclosed in detail. If a skilled artisan would have understood the inventor to be in possession of the claimed invention at the time of filing, even if every nuance of the claims is not explicitly described in the specification, then the adequate description requirement is met. (citations omitted.)

Thus, the written description standard is fulfilled by both what is specifically disclosed and what is conventional or well known to one skilled in the art.

SEQ ID NO:1 is specifically disclosed in the application (see, for example, pages 47-48 of the Sequence Listing). Variants of SEQ ID NO:1 are described, for example, at page 4, line 28 through page 5, line 1. In particular, the preferred, more preferred, and most preferred SEQ ID NO:1 variants (at least 80%, 90%, and at least 95% amino acid sequence similarity to SEQ ID NO:1) are described, for example, at page 11, lines 18-21. Incyte clones in which the nucleic acids encoding the human HTAP were first identified and libraries from which those clones were isolated are described, for example, at page 11, lines 1-6 of the Specification. Chemical and structural features of HTAP are described, for example, on page 11, lines 7-14. Given SEQ ID NO:1, one of ordinary skill in the art would recognize "a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1." The Specification describes (e.g., page 39, line 23 through page 40, line 13) how to use BLAST to determine whether a given sequence falls within the "at least 90% identical" scope. Immunogenic fragments are described in the Specification, e.g, at page 5, lines 26-28, page 25, lines 19-25, and page 45, lines 12-27.

There simply is no requirement that the claims recite particular variant and fragment polypeptide sequences because the claims already provide sufficient structural definition of the claimed subject matter. That is, the polypeptide variants and fragments are defined in terms of SEQ ID NO:1 ("An isolated polypeptide selected from the group consisting of: . . . b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1, and c) an immunogenic fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1." Because the polypeptide variants and fragments are defined in terms of SEQ ID NO:1, the precise chemical structure of every polypeptide variant and fragment within the scope of the claims can be discerned. The Examiner's position is nothing more than a misguided attempt to require Appellants to unduly limit the scope of their claimed invention. Appellants further submit that given the polypeptide sequence of SEQ ID NO:1, it would be redundant to list specific fragments. The structure of SEQ ID NO:1 provides the blueprint for all fragments thereof. Listing all possible fragments of SEQ ID NO:1 is, thus, a superfluous exercise which would needlessly clutter the Specification. As long as the

polypeptide variants and fragments are naturally-occurring, they are useful in toxicology testing. Their "function," whether the same or different than that of SEQ ID NO:1, is immaterial, given the description in the Specification and what is known to one of skill in the art (see, *infra*, Issue 2, Utility Rejection). Accordingly, the Specification provides an adequate written description of the recited polypeptides.

A. The present claims specifically define the claimed genus through the recitation of chemical structure

Court cases in which "DNA claims" have been at issue (which are hence relevant to claims to proteins encoded by the DNA) commonly emphasize that the recitation of structural features or chemical or physical properties are important factors to consider in a written description analysis of such claims. For example, in *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993), the court stated that:

> If a conception of a DNA requires a precise definition, such as by structure, formula, chemical name or physical properties, as we have held, then a description also requires that degree of specificity.

In a number of instances in which claims to DNA have been found invalid, the courts have noted that the claims attempted to define the claimed DNA in terms of functional characteristics without any reference to structural features. As set forth by the court in *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997):

> In claims to genetic material, however, a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA," without more, is not an adequate written description of the genus because it does not distinguish the claimed genus from others, except by function.

Thus, the mere recitation of functional characteristics of a DNA, without the definition of structural features, has been a common basis by which courts have found invalid claims to DNA. For example, in *Lilly*, 43 USPQ2d at 1407, the court found invalid for violation of the written description requirement the following claim of U.S. Patent No. 4,652,525:

> 1. A recombinant plasmid replicable in procaryotic host containing within its nucleotide sequence a subsequence having the structure of the reverse transcript of an mRNA of a vertebrate, which mRNA encodes insulin.

In *Fiers*, 25 USPQ2d at 1603, the parties were in an interference involving the following count:

> A DNA which consists essentially of a DNA which codes for a human fibroblast interferon-beta polypeptide.

Party Revel in the *Fiers* case argued that its foreign priority application contained an adequate written description of the DNA of the count because that application mentioned a potential method for isolating the DNA. The Revel priority application, however, did not have a description of any particular DNA structure corresponding to the DNA of the count. The court therefore found that the Revel priority application lacked an adequate written description of the subject matter of the count.

Thus, in *Lilly* and *Fiers*, nucleic acids were defined on the basis of functional characteristics and were found not to comply with the written description requirement of 35 U.S.C. §112; *i.e.*, "an mRNA of a vertebrate, which mRNA encodes insulin" in *Lilly*, and "DNA which codes for a human fibroblast interferon-beta polypeptide" in *Fiers*. In contrast to the situation in *Lilly* and *Fiers*, the claims at issue in the present application define polypeptides in terms of chemical structure, rather than on functional characteristics. For example, the "variant language" and "fragment language" of independent Claim 1 recites chemical structure to define the claimed genus:

> 1. An isolated polypeptide selected from the group consisting of: . . .
> b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1, and
> c) an immunogenic fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1.

From the above it should be apparent that the claims of the subject application are fundamentally different from those found invalid in *Lilly* and *Fiers*. The subject matter of the present claims is defined in terms of the chemical structure of SEQ ID NO:1. In the present case, there is no reliance merely on a description of functional characteristics of the polypeptides recited by the claims. Such functional recitations that are included add to the structural characterization of the recited polypeptides. The polypeptides defined in the claims of the present application recite structural features, and cases such as *Lilly* and *Fiers* stress that the

recitation of structure is an important factor to consider in a written description analysis of claims of this type. By failing to base its written description inquiry "on whatever is now claimed," the Final Office Action failed to provide an appropriate analysis of the present claims and how they differ from those found not to satisfy the written description requirement in *Lilly* and *Fiers*.

B. The present claims do not define a genus which is "highly diverse"

Furthermore, the claims at issue do not describe a genus which could be characterized as having "highly diverse functions." (Office Action mailed October 29, 2002, page 4.) Available evidence illustrates that the claimed genus is of narrow scope.

In support of this assertion, the Board's attention is directed to the enclosed reference by Brenner et al. ("Assessing sequence comparison methods with reliable structurally identified distant evolutionary relationships," Proc. Natl. Acad. Sci. USA (1998) 95:6073-6078) (Reference No. 1). Through exhaustive analysis of a data set of proteins with known structural and functional relationships and with <90% overall sequence identity, Brenner et al. have determined that 30% identity is a reliable threshold for establishing evolutionary homology between two sequences aligned over at least 150 residues. (Brenner et al., pages 6073 and 6076.) Furthermore, local identity is particularly important in this case for assessing the significance of the alignments, as Brenner et al. further report that ≥40% identity over at least 70 residues is reliable in signifying homology between proteins. (Brenner et al., page 6076.)

The present application is directed, *inter alia*, to proteins related to the amino acid sequence of SEQ ID NO:1. In accordance with Brenner et al, naturally occurring molecules may exist which could be characterized as tumorigenesis proteins and which have as little as 40% identity over at least 70 residues to SEQ ID NO:1. The "variant language" of the present claims recites, for example, polypeptides "comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1," (note that SEQ ID NO:1 has 195 amino acid residues). This variation is far less than that of all potential tumorigenesis proteins related to SEQ ID NO:1, i.e., those tumorigenesis proteins having as little as 40% identity over at least 70 residues to SEQ ID NO:1.

The Examiner disputes the evidence of the Brenner et al. paper, arguing that "Brenner et al. merely point out (page 6076, 2nd column, 2nd paragraph) that a 30% identity was a reliable

threshold for plotting the percent identity of unrelated proteins in a particular database- the PDB90D-B (Protein Data Bank comprising domains with were all less than 90% identical) which contains over 2000 protein domains - (page 6074, 2nd column, 2nd paragraph, and Figure 3). In contrast, applicant is comparing the sequence identity of an unknown protein to the sequence of BUP. Thus, from a statistical view, one of ordinary skill in the art would conclude that applicant does not have the quantity of data to extrapolate the results of Brenner et al." (Final Office Action, page 3.)

The Examiner appears to have misunderstood the significance of the Brenner et al. paper's findings. The Brenner et al. paper does not describe a method for figuring out functions of unknown proteins, The Brenner et al. paper evaluates known methods of sequence comparison using the SCOP data set of proteins whose functions are already known independently of sequence comparison methods. One does not need independently to come up with a new SCOP-sized data set to use the conclusions of the Brenner et al. paper, that sequence comparison methods are reliable in determining relationships between proteins and that at least 30% identity over at least 150 amino acid residues is a good cutoff value.

The SCOP database used in the Brenner et al. paper is a database of proteins with known structures. In the Brenner et al. paper the SCOP database was used to test the reliability of sequence comparison methods. The Brenner et al. paper does not discuss predicting "functional similarity", but rather evolutionary relationships. Use of this database of proteins with known structures allowed the authors to determine whether homologies predicted from the sequence comparison methods tested in the article were truly similar structurally. The Brenner et al. paper is not trying to predict relationships between proteins; the Brenner et al. paper is evaluating known methods of predicting protein relationships. One cannot test the ability of sequence comparison methods in predicting actual structural homology if one starts with protein sequences whose structures were not already known previously and independently of the sequence comparison.

The Examiner further contends that "Brenner et al. teach that high percent identity does not necessarily identify related proteins (Figure 2) wherein the principal reasons percentage identity does so poorly seem to be that is it ignores information about gaps and about the conservative or radical nature of residue substitutions (page 6076, 2nd column, 1st paragraph)." (Final Office Action, page 3.)

The Examiner appears to draw the incorrect conclusion from Figure 2 of the Brenner et al. paper with respect to its relevance to the reliability of the patent application's conclusion that the instant SEQ ID NO:1 polypeptide is related to the murine BUP protein, and that the polypeptide variants at least 90% identical to the SEQ ID NO:1 polypeptide are related to the SEQ ID NO:1 polypeptide, based on their percentage identity. Figure 2 of the Brenner et al. paper gives an example of "[u]nrelated proteins with high percentage identity." (Brenner et al., page 6075, Figure 2.) Hemoglobin β-chain (1hdsb) and cellulase E2 (1tml_) "have 39% identity over 64 residues, a level which is often believed to indicative of homology. Despite this high degree of identity, their structures strongly suggest that these proteins are not related." (Brenner et al. , page 6075, Figure 2.) Figure 2 of Brenner et al. paper does not support the Examiner's arguments for the following reasons. The percentage identity over sequence length for the alignment of the SEQ ID NO:1 polypeptide with respect to BUP, and for the alignment of the SEQ ID NO:1 polypeptide variants with respect to the SEQ ID NO:1 polypeptide is much higher than that for the alignment of hemoglobin and cellulase. The SEQ ID NO:1 polypeptide and BUP share 89% identity over 195 amino acid residues. The SEQ ID NO:1 polypeptide and its 90% variants share at least 90% identity over 195 amino acid residues. These percentage identity over sequence length values (89% over 195 amino acid residues and at least 90% over 195 amino acid residues) are much greater than those between hemoglobin and cellulase (39% over 64 amino acid residues). It is noted that the hemoglobin and cellulase example in Figure 2 does not meet the cutoffs taught in the Brenner et al. paper, i.e, that "30% identity is a reliable threshold for this database only for sequence alignments of at least 150 residues" and "it is probably necessary for alignments to be at least 70 residues in length before 40% is a reasonable threshold." (Brenner et al., page 6076.) These cutoffs were determined from the analysis summarized in Figure 3 of the Brenner et al. paper. Therefore it is more likely than not that the claimed SEQ ID NO:1 polypeptide is related to murine BUP and that the 90% variants of the SEQ ID NO:1 polypeptide are related to the SEQ ID NO:1 polypeptide.

The Examiner further cites Skolnick et al. as teaching that "the skilled artisan is well aware that assigning functional activities for any particular protein or family based upon sequence homology is inaccurate." (Office Action mailed October 29, 2002, page 4.) However, Skolnick et al. disclose that there are only 30-50% of proteins whose function cannot be assigned by any current methods (page 37, col. 2). This makes it more likely than not that the claimed

SEQ ID NO:1 polypeptide, which has 89% sequence identity to murine BUP, and the claimed polypeptide variants, which have at least 90% sequence identity to the SEQ ID NO:1 polypeptide, are among the group which can be properly annotated.

Moreover, Appellants note that it is well known in the art that sequence similarity is predictive of similarity in functional activity. Hegyi and Gerstein ("Annotation Transfer for Genomics: Measuring Functional Divergence in Multi-Domain Proteins," Genome Research (2001) 11: 1632-1640; Reference No. 2) conclude that "the probability that two single-domain proteins that have the same superfamily structure have the same function (whether enzymatic or not) is about 2/3." (Reference No. 2, page 1635.) Hegyi and Gerstein also conclude that, for multi-domain proteins with "almost complete coverage with exactly the same type and number of superfamilies, following each other in the same order" "[t]he probability that the functions are the same in this case was 91%." (Reference No. 2, page 1636.) Hegyi and Gerstein (Reference No. 2, page 1632) further note that

> Wilson et al. (2000) compared a large number of protein domains to one another in a pair-wise fashion with respect to similarities in sequence, structure, and function. Using a hybrid functional classification scheme merging the ENZYME and FlyBase systems (Gelbart et al. 1997; Bairoch 2000), they found that precise function is not conserved below 30–40% identity, although the broad functional class is usually preserved for sequence identities as low as 20–25%, given that the sequences have the same fold. Their survey also reinforced the previously established general exponential relationship between structural and sequence similarity (Chothia and Lesk 1986).

The claimed SEQ ID NO:1 polypeptide shares 89% sequence identity with murine BUP, and the claimed polypeptide variants share more than 90% sequence identity with the SEQ ID NO:1 polypeptide, well above the thresholds described in the Hegyi and Gerstein article (Reference No. 2) cited above. Therefore, there is a reasonable probability that the SEQ ID NO:1 polypeptide would have the same function as murine BUP and that the SEQ ID NO:1 polypeptide variants would have the same function as the SEQ ID NO:1 polypeptide.

Furthermore, if the Examiner is alleging that the "highly diverse" nature of the claimed genus is that the claimed polypeptide variants and fragments have different "functions" from SEQ ID NO:1, Appellants repeat that function is immaterial to the written description of the claimed polypeptides, given the description in the Specification and what is known to one of skill in the art. The written description describes polypeptides comprising a naturally-occurring amino

acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1 and immunogenic fragments of a polypeptide having an amino acid sequence of SEQ ID NO:1. As the claimed variants and fragments are not described by their having the same "function" as SEQ ID NO:1, the Examiner's arguments regarding "function" are not relevant to the written description issue. It is routine to calculate percentage identity. It is routine to use naturally-occurring polypeptides in toxicology testing. "Function" is irrelevant to the use of the claimed polypeptides in toxicology testing. (See *infra*, Issue 2, Utility Rejection.)

C. The state of the art at the time of the present invention is further advanced than at the time of the *Lilly* and *Fiers* applications

In the *Lilly* case, claims of U.S. Patent No. 4,652,525 were found invalid for failing to comply with the written description requirement of 35 U.S.C. §112. The '525 patent claimed the benefit of priority of two applications, Application Serial No. 801,343 filed May 27, 1977, and Application Serial No. 805,023 filed June 9, 1977. In the *Fiers* case, party Revel claimed the benefit of priority of an Israeli application filed on November 21, 1979. Thus, the written description inquiry in those case was based on the state of the art at essentially at the "dark ages" of recombinant DNA technology.

The present application has a priority date of March 20, 1997. Much has happened in the development of recombinant DNA technology in the 17 or more years from the time of filing of the applications involved in *Lilly* and *Fiers* and the present application. For example, the technique of polymerase chain reaction (PCR) was invented. Highly efficient cloning and DNA sequencing technology has been developed. Large databases of protein and nucleotide sequences have been compiled. Much of the raw material of the human and other genomes has been sequenced. With these remarkable advances one of skill in the art would recognize that, given the sequence information of SEQ ID NO:1, and the additional extensive detail provided by the subject application, the present inventors were in possession of the claimed polypeptide variants and fragments at the time of filing of this application.

D. Summary

The Final Office Action failed to base its written description inquiry "on whatever is now claimed." Consequently, the Action did not provide an appropriate analysis of the present claims and how they differ from those found not to satisfy the written description requirement in cases such as *Lilly* and *Fiers*. In particular, the claims of the subject application are fundamentally different from those found invalid in *Lilly* and *Fiers*. The subject matter of the present claims is defined in terms of the chemical structure of SEQ ID NO:1. The courts have stressed that structural features are important factors to consider in a written description analysis of claims to nucleic acids and proteins. In addition, the genus of polypeptides defined by the present claims is adequately described, as evidenced by Brenner et al. Furthermore, there have been remarkable advances in the state of the art since the *Lilly* and *Fiers* cases, and these advances were given no consideration whatsoever in the position set forth by the Final Office Action.

Issue 2Utility Rejection

Claims 1-2 and 15-16 stand rejected under 35 U.S.C. §§ 101 and 112, first paragraph, based on the allegation that the claimed invention lacks patentable utility. The rejection alleges in particular that "the claimed invention is not supported by either a specific and a substantial asserted utility or a well established utility." (Office Action mailed October 29, 2002, page 8.)

The rejection of Claims 1-2 and 15-16 is improper, as the inventions of those claims have a patentable utility as set forth in the instant specification, and/or a utility well-known to one of ordinary skill in the art.

The invention at issue, identified in the patent application as a human tumorigenesis protein, abbreviated as HTAP, is a polypeptide encoded by a gene that is expressed in human uterus. The novel polypeptide is demonstrated in the specification to be a tumorigenesis protein. The claimed invention has numerous practical, beneficial uses in toxicology testing, drug development, and the diagnosis of disease, none of which require knowledge of how the polypeptide actually functions. As a result of the benefits of these uses, the claimed invention already enjoys significant commercial success.

There is, in addition, direct proof of the utility of the claimed invention. Appellants previously submitted on January 29, 2003 the Declaration of Lars Michael Furness[2] describing some of the practical uses of the claimed invention in gene and protein expression monitoring applications as they would have been understood at the time of the patent application. The Furness Declaration describes, in particular, how the claimed polypeptide can be used in protein expression analysis techniques such as 2-D PAGE gels and western blots. Using the claimed invention with these techniques, persons of ordinary skill in the art can better assess, for example, the potential toxic effect of a drug candidate. (Furness Declaration at ¶ 10).

The Patent Examiner does not dispute that the claimed polypeptide can be used in 2-D PAGE gels and western blots to perform drug toxicity testing. Instead, the Patent Examiner contends that the claimed polypeptide cannot be useful without precise knowledge of its function. But the law never has required knowledge of biological function to prove utility. It is the claimed invention's uses, not its functions, that are the subject of a proper analysis under the utility requirement.

In any event, as demonstrated by the Furness Declaration, the person of ordinary skill in the art can achieve beneficial results from the claimed polypeptide in the absence of any knowledge as to the precise function of the polypeptide. The uses of the claimed polypeptide for gene expression monitoring applications including toxicology testing are in fact independent of its precise function.

I. The Applicable Legal Standard

To meet the utility requirement of sections 101 and 112 of the Patent Act, the patent applicant need only show that the claimed invention is "practically useful," *Anderson v. Natta*, 480 F.2d 1392, 1397, 178 USPQ 458 (CCPA 1973) and confers a "specific benefit" on the public. *Brenner v. Manson*, 383 U.S. 519, 534-35, 148 USPQ 689 (1966). As discussed in a recent Court of Appeals for the Federal Circuit case, this threshold is not high:

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[2]The Examiner notes "[a]s an aside" that "Dr. [*sic*] Furness is a consultant for Incyte Pharmaceuticals, Inc., the assignee for this application, and thus is a concerned party." (Final Office Action, page 7). This is irrelevant. The Examiner does not and cannot dispute that Mr. Furness is an expert in the art, and the Examiner has an obligation to consider the Declaration of Appellants' expert.

> An invention is "useful" under section 101 if it is capable of providing some identifiable benefit. See *Brenner v. Manson*, 383 U.S. 519, 534 [148 USPQ 689] (1966); *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571 [24 USPQ2d 1401] (Fed. Cir. 1992) ("to violate Section 101 the claimed device must be totally incapable of achieving a useful result"); *Fuller v. Berger*, 120 F. 274, 275 (7th Cir. 1903) (test for utility is whether invention "is incapable of serving any beneficial end").

Juicy Whip Inc. v. Orange Bang Inc., 51 USPQ2d 1700 (Fed. Cir. 1999).

While an asserted utility must be described with specificity, the patent applicant need not demonstrate utility to a certainty. In *Stiftung v. Renishaw PLC*, 945 F.2d 1173, 1180, 20 USPQ2d 1094 (Fed. Cir. 1991), the United States Court of Appeals for the Federal Circuit explained:

> An invention need not be the best or only way to accomplish a certain result, and it need only be useful to some extent and in certain applications: "[T]he fact that an invention has only limited utility and is only operable in certain applications is not grounds for finding lack of utility." *Envirotech Corp. v. Al George, Inc.*, 730 F.2d 753, 762, 221 USPQ 473, 480 (Fed. Cir. 1984).

The specificity requirement is not, therefore, an onerous one. If the asserted utility is described so that a person of ordinary skill in the art would understand how to use the claimed invention, it is sufficiently specific. *See Standard Oil Co. v. Montedison, S.p.a.*, 212 U.S.P.Q. 327, 343 (3d Cir. 1981). The specificity requirement is met unless the asserted utility amounts to a "nebulous expression" such as "biological activity" or "biological properties" that does not convey meaningful information about the utility of what is being claimed. *Cross* v. *Iizuka*, 753 F.2d 1040, 1048 (Fed. Cir. 1985).

In addition to conferring a specific benefit on the public, the benefit must also be "substantial." *Brenner*, 383 U.S. at 534. A "substantial" utility is a practical, "real-world" utility. *Nelson v. Bowler*, 626 F.2d 853, 856, 206 USPQ 881 (CCPA 1980).

If persons of ordinary skill in the art would understand that there is a "well-established" utility for the claimed invention, the threshold is met automatically and the applicant need not make any showing to demonstrate utility. Manual of Patent Examination Procedure at § 706.03(a). Only if there is no "well-established" utility for the claimed invention must the applicant demonstrate the practical benefits of the invention. *Id.*

Once the patent applicant identifies a specific utility, the claimed invention is presumed to possess it. *In re Cortright*, 165 F.3d 1353, 1357, 49 USPQ2d 1464 (Fed. Cir. 1999); *In re Brana*, 51 F.3d 1560, 1566; 34 USPQ2d 1436 (Fed. Cir. 1995). In that case, the Patent Office bears the burden of demonstrating that a person of ordinary skill in the art would reasonably doubt that the asserted utility could be achieved by the claimed invention. *Id.* To do so, the Patent Office must provide evidence or sound scientific reasoning. *See In re Langer*, 503 F.2d 1380, 1391-92, 183 USPQ 288 (CCPA 1974). If and only if the Patent Office makes such a showing, the burden shifts to the applicant to provide rebuttal evidence that would convince the person of ordinary skill that there is sufficient proof of utility. *Brana*, 51 F.3d at 1566. The applicant need only prove a "substantial likelihood" of utility; certainty is not required. *Brenner*, 383 U.S. at 532.

II. Uses of the claimed polypeptide for diagnosis of conditions and disorders characterized by expression of HTAP, for toxicology testing, and for drug discovery are sufficient utilities under 35 U.S.C. §§ 101 and 112, first paragraph

The claimed invention meets all of the necessary requirements for establishing a credible utility under the Patent Law: There are "well-established" uses for the claimed invention known to persons of ordinary skill in the art, and there are specific practical and beneficial uses for the invention disclosed in the patent application's specification. These uses are explained, in detail, in the previously submitted Furness Declaration. Objective evidence further corroborates the credibility of the asserted utilities.

A. The similarity of the claimed polypeptide to murine lymphomagenesis-associated protein, BUP, demonstrates utility

Because there is a substantial likelihood that the claimed HTAP is functionally related to murine lymphomagenesis-associated protein, BUP, there is by implication a substantial likelihood that the claimed polypeptide is similarly useful. Appellants need not show any more to demonstrate utility. *In re Brana*, 51 F.3d at 1567.

It is undisputed, and readily apparent from the patent application, that the claimed polypeptide shares 89% sequence identity over 195 amino acid residues with murine

lymphomagenesis-associated protein, BUP. This is more than enough homology to demonstrate a reasonable probability that the utility of murine lymphomagenesis-associated protein, BUP, can be imputed to the claimed invention. It is well-known that the probability that two unrelated polypeptides share more than 40% sequence homology over 70 amino acid residues is exceedingly small. (Brenner et. al., *supra* Reference No. 1.) Given homology in excess of 40% over many more than 70 amino acid residues, the probability that the claimed polypeptide is related to murine lymphomagenesis-associated protein, BUP, is, accordingly, very high.

The Examiner must accept the Appellants' demonstration that the homology between the claimed invention and murine lymphomagenesis-associated protein, BUP, demonstrates utility by a reasonable probability unless the Examiner can demonstrate through evidence or sound scientific reasoning that a person of ordinary skill in the art would doubt utility. *See In re Langer*, 503 F.2d 1380, 1391-92, 183 USPQ 288 (CCPA 1974). The Examiner has not provided sufficient evidence or sound scientific reasoning to the contrary.

The Examiner states that "Applicant argues that similarity of the claimed polypeptide to BUP. These arguments have been addressed above." (Final Office Action, page 5.) Appellants assume that the Examiner is referring to the arguments that the Examiner made, with respect to the written description rejection, regarding percentage identity and similarity between proteins. For at least the reasons discussed *supra* under Issue 1, Written Description Rejection, there is a reasonable probability that the SEQ ID NO:1 polypeptide shares the same function as murine BUP and that the claimed polypeptide variants share the same function as the SEQ ID NO:1 polypeptide.

While the Examiner has cited literature (Skolnick et al., and Brenner et al.) identifying some of the difficulties that may be involved in predicting protein function, none suggest that functional homology cannot be inferred by a reasonable probability in this case. For at least the reasons discussed *supra* under Issue 1, Written Description Rejection, there is a reasonable probability that the SEQ ID NO:1 polypeptide shares the same function as murine BUP and that the claimed polypeptide variants share the same function as the SEQ ID NO:1 polypeptide. At most, these articles individually and together stand for the proposition that it is difficult to make predictions about function with certainty. The standard applicable in this case is not, however, proof to certainty, but rather proof to reasonable probability.

B. The uses of HTAP for toxicology testing, drug discovery, and disease diagnosis are practical uses that confer "specific benefits" to the public

The claimed invention has specific, substantial, real-world utility by virtue of its use in toxicology testing, drug development and disease diagnosis through gene expression profiling. These uses are explained in detail in the previously submitted Furness Declaration. The claimed invention is a useful tool in two-dimensional polyacrylamide gel electrophoresis ("2-D PAGE") analysis and western blots used to monitor protein expression and assess drug toxicity.

The instant application is a continuation application of and claimed priority to United States patent application Serial No. 09/183,825 filed on October 30, 1998), which in turn was a divisional application of and claimed priority to United States patent application Serial No. 08/822,260 filed on March 20, 1997 (hereinafter "the Hillman '260 application"), having essentially the identical specification, with the exception of corrected typographical errors and reformatting changes. Thus page and line numbers may not match as between the Hillman '915 application and the Hillman '260 application.

In his Declaration, Mr. Furness explains the many reasons why a person skilled in the art who read the Hillman '260 application on March 20, 1997 would have understood that application to disclose the claimed polypeptide to be useful for a number of gene and protein expression monitoring applications, *e.g.*, in 2-D PAGE technologies, in connection with the development of drugs and the monitoring of the activity of such drugs. (Furness Declaration at, e.g., ¶¶ 10-13). Much, but not all, of Mr. Furness' explanation concerns the use of the claimed polypeptide in the creation of protein expression maps using 2-D PAGE.

2-D PAGE technologies were developed during the 1980's. Since the early 1990's, 2-D PAGE has been used to create maps showing the differential expression of proteins in different cell types or in similar cell types in response to drugs and potential toxic agents. Each expression pattern reveals the state of a tissue or cell type in its given environment, *e.g.*, in the presence or absence of a drug. By comparing a map of cells treated with a potential drug candidate to a map of cells not treated with the candidate, for example, the potential toxicity of a drug can be assessed. (Furness Declaration at ¶ 10.)

The claimed invention makes 2-D PAGE analysis a more powerful tool for toxicology and drug efficacy testing. A person of ordinary skill in the art can derive more information about the state or states or tissue or cell samples from 2-D PAGE analysis with the claimed invention than without it. As Mr. Furness explains:

> In view of the Hillman '260 application. . . and other related pre-March 20, 1997 publications, persons skilled in the art on March 20, 1997 clearly would have understood the Hillman '260 application to disclose the SEQ ID NO:1 polypeptide to be useful in 2-D PAGE analyses for the development of new drugs and monitoring the activities of drugs for such purposes as evaluating their efficacy and toxicity. . . . (Furness Declaration, ¶ 10)
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> * * *
>
> Persons skilled in the art would appreciate that a 2-D PAGE map that utilized the SEQ ID NO:1 polypeptide sequence would be a more useful tool than a 2-D PAGE map that did not utilize this protein sequence in connection with conducting protein expression monitoring studies on proposed (or actual) drugs for treating disorders associated with cell proliferation and inflammation for such purposes as evaluating their efficacy and toxicity. (Furness Declaration, ¶ 12)

Mr. Furness' observations are confirmed in the literature published before the filing of the patent application. Wilkins, for example, describes how 2-D gels are used to define proteins present in various tissues and measure their levels of expression, the data from which is in turn used in databases:

> For proteome projects, the aim of [computer-aided 2-D PAGE] analysis . . . is to catalogue all spots from the 2-D gel in a qualitative and if possible quantitative manner, so as to define the number of proteins present and their levels of expression. Reference gel images, constructed from one or more gels, form the basis of two-dimensional gel databases. (Wilkins, Tab C, page 26).

C. The use of proteins expressed by humans as tools for toxicology testing, drug discovery, and the diagnosis of disease is now "well-established"

The technologies made possible by expression profiling using polypeptides are now well-established. The technical literature recognizes not only the prevalence of these technologies, but also their unprecedented advantages in drug development, testing and safety assessment. These technologies include toxicology testing, as described by Furness in his Declaration.

Toxicology testing is now standard practice in the pharmaceutical industry. See, *e.g.*, John C. Rockett, et. al., Differential gene expression in drug metabolism and toxicology: practicalities, problems, and potential, Xenobiotica 29:655-691 (July 1999) (Reference No. 3):

> Knowledge of toxin-dependent regulation in target tissues is not solely an academic pursuit as much interest has been generated in the pharmaceutical industry to harness this technology in the early identification of toxic drug candidates, thereby shortening the developmental process and contributing substantially to the safety assessment of new drugs. ((Reference No. 3), page 656)

To the same effect are several other scientific publications, including Emile F. Nuwaysir, et al., Microarrays and Toxicology: The Advent of Toxicogenomics, Molecular Carcinogenesis 24:153-159 (1999) (Reference No. 4); Sandra Steiner and N. Leigh Anderson, Expression profiling in toxicology -- potentials and limitations, Toxicology Letters 112-13:467-471 (2000) (Reference No. 5).

The more genes – and, accordingly, the polypeptides they encode -- that are available for use in toxicology testing, the more powerful the technique. Control genes are carefully selected for their stability across a large set of array experiments in order to best study the effect of toxicological compounds. See attached email from the primary investigator of the Nuwaysir paper, Dr. Cynthia Afshari to an Incyte employee, dated July 3, 2000, as well as the original message to which she was responding (Reference No. 6). Thus, there is no expressed gene which is irrelevant to screening for toxicological effects, and all expressed genes have a utility for toxicological screening.

In fact, the potential benefit to the public, in terms of lives saved and reduced health care costs, are enormous. Recent developments provide evidence that the benefits of this information are already beginning to manifest themselves. Examples include the following:

- In 1999, CV Therapeutics, an Incyte collaborator, was able to use Incyte gene expression technology, information about the structure of a known transporter gene, and chromosomal mapping location, to identify the key gene associated with Tangier disease. This discovery took place over a matter of only a few weeks, due to the power of these new genomics technologies. The discovery received an award from the American Heart Association as one of the top 10 discoveries associated with heart disease research in 1999.

- In an April 9, 2000, article published by the Bloomberg news service, an Incyte customer stated that it had reduced the time associated with target discovery and validation from 36 months to 18 months, through use of Incyte's genomic

information database. Other Incyte customers have privately reported similar experiences. The implications of this significant saving of time and expense for the number of drugs that may be developed and their cost are obvious.

- In a February 10, 2000, article in the *Wall Street Journal*, one Incyte customer stated that over 50 percent of the drug targets in its current pipeline were derived from the Incyte database. Other Incyte customers have privately reported similar experiences. By doubling the number of targets available to pharmaceutical researchers, Incyte genomic information has demonstrably accelerated the development of new drugs.

Because the Examiner failed to address or consider the "well-established" utilities for the claimed invention in toxicology testing, drug development, and the diagnosis of disease, the Examiner's rejections should be overturned regardless of their merit.

D. Objective evidence corroborates the utilities of the claimed invention

There is in fact no restriction on the kinds of evidence a Patent Examiner may consider in determining whether a "real-world" utility exists. "Real-world" evidence, such as evidence showing actual use or commercial success of the invention, can demonstrate conclusive proof of utility. *Raytheon v. Roper*, 220 USPQ2d 592 (Fed. Cir. 1983); *Nestle v. Eugene*, 55 F.2d 854, 856, 12 USPQ 335 (6th Cir. 1932). Indeed, proof that the invention is made, used or sold by any person or entity other than the patentee is conclusive proof of utility. *United States Steel Corp.* v. *Phillips Petroleum Co.*, 865 F.2d 1247, 1252, 9 USPQ2d 1461 (Fed. Cir. 1989).

Over the past several years, a vibrant market has developed for databases containing the sequences of all expressed genes (along with the polypeptide translations of those genes). (Note that the value in these databases is enhanced by their completeness, but each sequence in them is independently valuable.) The databases sold by Appellants' assignee, Incyte, include exactly the kinds of information made possible by the claimed invention, such as tissue and disease associations. Incyte sells its database containing the sequence of the claimed polypeptide and millions of other sequences throughout the scientific community, including to pharmaceutical companies who use the information to develop new pharmaceuticals.

Both Incyte's customers and the scientific community have acknowledged that Incyte's databases have proven to be valuable in, for example, the identification and development of drug candidates. As Incyte adds information to its databases, including the information that can be

generated only as a result of Incyte's discovery of the claimed polypeptide, the databases become even more powerful tools. Thus the claimed invention adds more than incremental benefit to the drug discovery and development process.

III. The Patent Examiner's Rejections Are Without Merit

Rather than responding to the evidence demonstrating utility, the Examiner attempts to dismiss it altogether by arguing that the disclosed and well-established utilities for the claimed polypeptide are not "credible, specific, or substantial" utilities. (Office Action mailed October 29, 2002, page 8.) The Examiner is incorrect both as a matter of law and as a matter of fact.

A. The Precise Biological Role Or Function Of An Expressed Polypeptide Is Not Required To Demonstrate Utility

The Patent Examiner's primary rejection of the claimed invention is based on the ground that, without information as to the precise "functional characterization" of the claimed invention, the claimed invention's utility is not sufficiently specific. (Office Action mailed October 29, 2002, page 8.) According to the Examiner, it is not enough that a person of ordinary skill in the art could use and, in fact, would want to use the claimed invention either by itself or in a 2-D gel or western blot to monitor the expression of genes for such applications as the evaluation of a drug's efficacy and toxicity. The Examiner would require, in addition, that Appellants provide a specific and substantial interpretation of the results generated in any given expression analysis.

It may be that specific and substantial interpretations and detailed information on biological function are necessary to satisfy the requirements for publication in some technical journals, but they are not necessary to satisfy the requirements for obtaining a United States patent. The relevant question is not, as the Examiner would have it, whether it is known how or why the invention works, *In re Cortwright*, 165 F.3d 1353, 1359 (Fed. Cir. 1999), but rather whether the invention provides an "identifiable benefit" in presently available form. *Juicy Whip Inc.* v. *Orange Bang Inc.*, 185 F.3d 1364, 1366 (Fed. Cir. 1999). If the benefit exists, and there is a substantial likelihood the invention provides the benefit, it is useful. There can be no doubt, particularly in view of the Furness Declaration (at, *e.g.*, ¶¶ 10-13), that the present invention meets this test.

The threshold for determining whether an invention produces an identifiable benefit is low. *Juicy Whip*, 185 F.3d at 1366. Only those utilities that are so nebulous that a person of

ordinary skill in the art would not know how to achieve an identifiable benefit and, at least according to the PTO guidelines, so-called "throwaway" utilities that are not directed to a person of ordinary skill in the art at all, do not meet the statutory requirement of utility. Utility Examination Guidelines, 66 Fed. Reg. 1092 (Jan. 5, 2001).

Knowledge of the biological function or role of a biological molecule has never been required to show real-world benefit. In its most recent explanation of its own utility guidelines, the PTO acknowledged as much (66 F.R. at 1095):

> [T]he utility of a claimed DNA does not necessarily depend on the function of the encoded gene product. A claimed DNA may have specific and substantial utility because, *e.g.*, it hybridizes near a disease-associated gene or it has gene-regulating activity.

By implicitly requiring knowledge of biological function for any claimed polypeptide, the Examiner has, contrary to law, elevated what is at most an evidentiary factor into an absolute requirement of utility. Rather than looking to the biological role or function of the claimed invention, the Examiner should have looked first to the benefits it is alleged to provide.

B. Membership in a Class of Useful Products Can Be Proof of Utility

Despite the uncontradicted evidence that the claimed polypeptide is a polypeptide expressed by humans, the Examiner refused to impute the utility of the members of the family of polypeptides expressed by humans to HTAP.

In order to demonstrate utility by membership in a class, the law requires only that the class not contain a substantial number of useless members. So long as the class does not contain a substantial number of useless members, there is sufficient likelihood that the claimed invention will have utility and a rejection under 35 U.S.C. § 101 is improper. That is true regardless of how the claimed invention ultimately is used and whether the members of the class possess one utility or many. *See Brenner* v. *Manson*, 383 U.S. 519, 532 (1966); *Application of Kirk*, 376 F.2d 936, 943 (CCPA 1967).

Membership in a "general" class is insufficient to demonstrate utility only if the class contains a substantial number of useless members. There would be, in that case, a substantial likelihood that the claimed invention is one of the useless members of the class. In the few cases in which class membership did not prove utility by substantial likelihood, the classes did in fact

include predominately useless members. *E.g.*, *Brenner* (man-made steroids); *Kirk* (same); *Natta* (man-made polyethylene polymers).[3]

The Examiner addresses HTAP as if the general class in which it is included is not the family of polypeptides expressed by humans, but rather all polypeptides, including the vast majority of useless theoretical molecules not occurring in nature, and thus not pre-selected by nature to be useful. While these "general classes" may contain a substantial number of useless members, the family of polypeptides expressed by humans does not. The family of polypeptides expressed by humans is sufficiently specific to rule out any reasonable possibility that HTAP would not also be useful like the other members of the family.

Because the Examiner has not presented any evidence that the family of polypeptides expressed by humans has any, let alone a substantial number, of useless members, the Examiner must conclude that there is a "substantial likelihood" that the claimed HTAP polypeptide is useful.

As demonstrated by Appellants, knowledge that HTAP is a polypeptide expressed by humans is more than sufficient to make it useful for the diagnosis and treatment of disorders associated with cell proliferation and inflammation. Indeed, HTAP has been shown to be expressed in libraries derived from tissues that are immortalized or cancerous, are associated with inflammation, and are associated with normal growth and development occurring in tissues of a fetus or child. The Examiner must accept these facts to be true unless the Examiner can provide evidence or sound scientific reasoning to the contrary. But the Examiner has not done so.

C. The uses of HTAP in toxicology testing, drug discovery, and disease diagnosis are practical uses beyond mere study of the invention itself

There is no authority for the proposition that use as a tool for research is not a substantial utility. Indeed, the Patent Office itself has recognized that just because an invention is used in a research setting does not mean that it lacks utility (Section 2107.01 of the Manual of Patent

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[3]At a recent Biotechnology Customer Partnership Meeting, PTO Senior Examiner James Martinell described an analytical framework roughly consistent with this analysis. He stated that when an applicant's claimed protein "is a member of a family of proteins that already are known based upon sequence homology," that can be an effective assertion of utility.

Examining Procedure, 8th Edition, August 2001, under the heading I. Specific and Substantial Requirements, Research Tools):

> Many research tools such as gas chromatographs, screening assays, and nucleotide sequencing techniques have a clear, specific and unquestionable utility (e.g., they are useful in analyzing compounds). An assessment that focuses on whether an invention is useful only in a research setting thus does not address whether the specific invention is in fact "useful" in a patent sense. Instead, Office personnel must distinguish between inventions that have a specifically identified substantial utility and inventions whose asserted utility requires further research to identify or reasonably confirm.

The PTO's actual practice has been, at least until the present, consistent with that approach. It has routinely issued patents for inventions whose only use is to facilitate research, such as DNA ligases, acknowledged by the PTO's Training Materials to be useful.

The subset of research uses that are not "substantial" utilities is limited. It consists only of those uses in which the claimed invention is to be an **object** of further study, thus merely inviting further research on the invention itself. This follows from *Brenner*, in which the U.S. Supreme Court held that a process for making a compound does not confer a substantial benefit where the only known use of the compound was to be the object of further research to determine its use. *Id.* at 535. Similarly, in *Kirk*, the Court held that a compound would not confer substantial benefit on the public merely because it might be used to synthesize some other, unknown compound that would confer substantial benefit. *Kirk*, 376 F.2d at 940, 945. ("What appellants are really saying to those in the art is take these steroids, experiment, and find what use they do have as medicines.") Nowhere do those cases state or imply, however, that a material cannot be patentable if it has some other, additional beneficial use in research.

Such beneficial uses beyond studying the claimed invention itself have been demonstrated, in particular those described in the Furness Declaration. The Furness Declaration demonstrates that the claimed invention is a tool, rather than an object, of research, and it demonstrates exactly how that tool is used. Without the claimed invention, it would be more difficult to generate information regarding the properties of tissues, cells, drug candidates and toxins apart from additional information about the polypeptide itself. (See the Furness Declaration, e.g, at ¶¶ 10-13.)

The claimed invention has numerous other uses as a research tool, each of which alone is a "substantial utility." These include in diagnostic assays and in drug screening (Specification, e.g., page 33, lines 8-16 and page 37, line 18 through page 38, line 6).

D. The Patent Examiner Failed to Demonstrate That a Person of Ordinary Skill in the Art Would Reasonably Doubt the Utility of the Claimed Invention

1. Biological function, significance, or activity is irrelevant to utility

The Examiner disputes the arguments made in the Furness Declaration on the utility of the claimed polypeptide in toxicology testing, stating that "no new facts or evidence on the role, function, or properties of the claimed protein have been presented." (Final Office Action, page 7.) The Examiner further alleged that "the specification provides no functional characterization of SEQ ID NO:1." (Office Action mailed October 29, 2002, page 8.) The Examiner also alleges that toxicology testing, "in the absence of any known role of NHT [*sic*], is considered to be further research on NHT [*sic*] itself, to determine the role, function, and properties of the protein." [4] (Final Office Action, page 7.) Appellants have demonstrated a utility for the claimed polypeptide irrespective of whether or not a person would wish to perform additional experimentation on biological "role, function, or properties" as another utility. The fact that additional experimentation could be performed to determine the functionality of the claimed polypeptide does not preclude, and is in fact irrelevant to, the actual utility of the invention. That utility exists today regardless of the specific function of the claimed polypeptide. The Examiner confuses use with function.

2. Irrelevance of tissue distribution or disease association to utility in toxicology testing

The Examiner argues on page 8 of the Office Action mailed October 29, 2002 that the specification does not disclose a "specific tissue distribution" of the claimed polypeptide or a "specific disease state in which these proteins affect." In the Final Office Action the Examiner further argues that "the specification does not establish that the protein of SEQ ID NO:1 is expressed in any eating disorder [*sic*] in any way that is different from the way it is expressed in

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[4]Appellants note that the Specification does not recite "NHT." The Examiner indicated in the Advisory Action that the use of the term "NHT" in the Final Office Action was a "typo." (Advisory Action, page 2.)

normal individuals."[5] (Final Office Action, page 7.) These are irrelevant. Appellants need not demonstrate whether the claimed polypeptide is associated with any tissue or disease, only whether the claimed polypeptide is useful. The claimed polypeptide is useful whether or not the claimed polypeptide is associated with any tissue or disease.

The claimed polypeptide can be used for toxicology testing in drug discovery without any knowledge of tissue distribution or disease association of the claimed polypeptide. Monitoring the expression of the claimed polypeptide gives important information on the potential toxicity of a drug candidate that is specifically targeted to any other polypeptide, regardless of the tissue distribution or disease association of the claimed polypeptide. The claimed polypeptide is useful for measuring the toxicity of drug candidates specifically targeted to **other** polypeptides regardless of any possible utility for measuring the properties of the claimed polypeptide.

Appellants note that monitoring the expression of the recited polypeptides is a method of testing the toxicology of drug candidates during the drug development process. If the expression of a particular polypeptide is affected in any way by exposure to a test compound, and if that particular polypeptide is not the specific target of the test compound (e.g., if the test compound is a drug candidate), then the change in expression is an indication that the test compound may have undesirable toxic side effects that may limit its usefulness as a specific drug. Toxicology testing using expression profiling using 2-D PAGE reduces time needed for drug development by weeding out compounds which are not specific to the drug target. Learning this from a 2-D PAGE gel in a protein expression monitoring experiment early in the drug development process costs less than learning this, for example, during Phase III clinical trials. It is important to note that such an indication of possible toxicity is specific not only for each compound tested, but also for each and every individual polypeptide whose expression is being monitored.

3. Use of the claimed polypeptide in toxicology testing

The Examiner argues that Appellants' arguments and the Furness Declaration are "not found persuasive" because "the type of testing discussed by Dr. [*sic*] Furness can be done with

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[5]Appellants note that the Specification does not recite "eating disorder." The Examiner indicated in the Advisory Action that the use of the phrase "eating disorder" in the Final Office Action was a "typo." (Advisory Action, page 2.)

any new, uncharacterized protein" and thus "the asserted utility is not specific." (Final Office Action, pages 6 and 7.) The Examiner further argued that "since the specification does not disclose a correlation between any disease state and an alteration in level or form of protein of SEQ ID NO:1, significant further experimentation would be required of the skilled artisan to establish such a correlation" and thus the utility is "not substantial." (Final Office Action, page 7.)

The Examiner's arguments amount to nothing more than the Examiner's disagreement with the Furness Declaration and the Appellants' assertions about the knowledge of a person of ordinary skill in the art, and is tantamount to the substitution of the Examiner's own judgment for that of the Appellants' expert. The Examiner must accept the Appellants' assertions to be true. The Examiner is, moreover, wrong on the facts because the Furness Declaration demonstrates how one of skill in the art, reading the Specification at the time the Hillman '260 application was filed (March 20, 1997), would have understood that Specification to disclose the use of the claimed polypeptide in gene expression monitoring for toxicology testing, drug development, and the diagnosis of disease (See the Furness Declaration at, e.g., ¶¶ 9-13).

For example, detecting the expression of the SEQ ID NO:1 polypeptide is a method of testing the toxicology of drug candidates during the drug development process. Mr. Furness in his Declaration states that "good drugs are not only potent, they are specific. This means that they have strong effects on a specific biological target and minimal effects on all other biological targets." (Furness Declaration ¶ 10.) Thus, if the expression of a particular polypeptide is affected in any way by exposure to a test compound, and if that particular polypeptide is not the specific target of the test compound (e.g., if the test compound is a drug candidate), then the change in expression is an indication that the test compound has undesirable toxic side effects. It is important to note that such an indication of possible toxicity is specific not only for each compound tested, but also for each and every individual polypeptide whose expression is being monitored.

However, the Examiner continues to view the utility in toxicology testing of the claimed polypeptide as requiring knowledge of either the biological function or disease association of the claimed polypeptide. The Examiner views toxicology testing as a process to measure the toxicity of a drug candidate only when that drug candidate is specifically targeted to the claimed

polypeptide. The Examiner has refused to consider that the claimed polypeptide is useful for measuring the toxicity of drug candidates which are targeted not to the claimed polypeptide, but to **other** polypeptides. This utility of the claimed polypeptide does not require any knowledge of the biological function or disease association of the SEQ ID NO:1 polypeptide and is a specific, substantial and credible utility.

The use of the claimed invention as a research tool in toxicology testing is specific and substantial. While it is true that all polypeptides expressed in humans have utility in toxicology testing based on the property of being expressed at some time in development or in the cell life cycle, this basis for utility does not preclude that utility from being specific and substantial. A toxicology test using any particular expressed polypeptide is dependent on the **identity** of that polypeptide, not on its biological function or its disease association. The results obtained from using any particular human-expressed polypeptide in toxicology testing are specific to both the compound being tested and the polypeptide used in the test. **No two human-expressed polypeptides are interchangeable for toxicology testing** because the effects on the expression of any two such polypeptides will differ depending on the identity of the compound tested and the **identities** of the two polypeptides. It is not necessary to know the biological functions and disease associations of the polypeptides in order to carry out such toxicology tests. Therefore, at the very least, the claimed polypeptide is a specific control for toxicology tests in developing drugs targeted to other polypeptides, and it is clearly useful as such.

4. The claimed isolated polypeptide is useful in toxicology testing

The Examiner further disputes the utility of the claimed polypeptide in toxicology testing, asserting that "the uses urged by Declarant do not require isolated protein of SEQ ID NO:1," and that "[i]n the types of analyses urged by Declarant, the proteins themselves are not isolated, nor are antibodies to specific proteins made." (Final Office Action, page 7.) However, the Examiner is incorrect in the assertion that an "isolated protein of SEQ ID NO:1" does not have utility in toxicology testing, for example, in 2-D PAGE analysis. The claimed isolated polypeptides are useful in toxicology testing in 2-D PAGE analyses, to identify which spot in the 2-D PAGE analysis of a biological sample corresponds to the sample-derived SEQ ID NO:1 polypeptide. For example, comigration of the known isolated SEQ ID NO:1 polypeptide with an

unknown sample spot on a 2-D PAGE gel identifies that unknown sample spot as sample-derived SEQ ID NO:1 polypeptide. In another example, the isolated SEQ ID NO:1 polypeptide may be used as an immunogen for the production of antibodies which can be used to detect sample-derived SEQ ID NO:1 polypeptide on the 2-D PAGE gel.

Such uses are supported, for example, in the Furness Declaration and in the Celis et al. article (Tab D) cited in the Furness Declaration. Furness in his Declaration states that "[e]xpressed proteins are useful for 2-D PAGE analysis in toxicology expression studies for a variety of reasons, particularly for purposes relating to providing controls for the 2-D PAGE analysis, and for identifying sequence or post-translational variants of the expressed sequences in response to exogenous compounds" and "[t]he isolated polypeptide could therefore be used as a control to more accurately gauge the expression of HTAP in the sample and consequently more accurately gauge the affect of a toxicant on expression of the gene." (Furness Declaration, ¶ 12)

Furthermore, Celis et al. (Tab D cited in the Furness Declaration; Reference No. 7 in this Appeal Brief) state that:

> A major obstacle encountered in building comprehensive 2-dimensional gel protein databases is identifying the large number of proteins separated by this technology. . . known proteins are identified by one or a combination of the following procedures: 1) **comigration with known proteins**, 2) **2-dimensional gel immunoblotting using specific antibodies**, 3) microsequencing. . . (Celis et al., page 2204, last paragraph in first column, emphasis added.)

> . . . we have received nearly 550 antibodies from laboratories all over the world and these are being systematically tested by 2-dimensional gel immunoblotting for antigen determination. . . . purified proteins and organelles provided by several laboratories have greatly aided identification of unknown proteins. (Celis et al., page 2204, first paragraph in second column.)

Therefore, the claimed isolated SEQ ID NO:1 polypeptide facilitates the detection and quantification of the expression of sample-derived SEQ ID NO:1 polypeptide. Such analysis allows one to determine whether the expression of the SEQ ID NO:1 polypeptide is affected by a test compound, as this can be a measure of possible toxicity of that test compound.

5. Utility of all expressed polypeptides in toxicology testing

The Examiner argues that use of the claimed polypeptide in toxicology testing is not acceptable because "this is a utility which would apply to virtually every member of a general class of materials, such as any collection of proteins or DNA" and that "such a utility is not specific." (Final Office Action, page 4.) The Examiner does not point to any law, however, that says a utility that is shared by a large class is somehow not a utility. If all of the class of expressed polypeptides can be so used, then they all have utility. The issue is, once again, whether the claimed polypeptide has any utility, not whether other compounds have a similar utility. Nothing in the law says that an invention must have a "unique" utility. Indeed, the whole notion of well-established" utilities PRESUPPOSES that many different inventions can have the exact same utility (if the Examiner's argument were correct, there could never be a well-established utility, because you could always find a generic group with the same utility!).

It is true that just about any expressed polypeptide will have use as a toxicology control, but Appellants need not argue this for the purposes of this case. Appellants argue only that the claimed polypeptide could be so used, and has provided the declaration of Furness to back this up. The point is not whether or not the claimed polypeptide is, in any given toxicology test, differentially expressed. The point is that the claimed polypeptide provides a useful measuring stick regardless of whether there is or is not differential expression. That makes the invention useful today, in the real-world, for real purposes.

6. Discussion of toxicology testing in the Specification

The Examiner alleges that "toxicology testing is not specifically recited in the specification as originally filed." (Final Office Action, page 4.) Well-established utilities, such as toxicology testing by the use of two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) maps, need not be explicitly disclosed in a patent application. Furthermore, the Examiner's position amounts to nothing more than the Examiner's disagreement with the Furness Declaration (which purports therefore to substitute the Examiner's judgment for that of Appellants' expert) and Appellants' assertions about the knowledge of a person of ordinary skill. The Examiner must accept Appellants' assertions to be true. The Final Office Action fails to address the disclosure in the instant Specification on gene and protein expression monitoring applications, as discussed below.

Support for the utility of the claimed polypeptide in toxicology testing, as well as for utility in drug screening, may be found in the Specification. For example, "protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies" may be used "for the detection and/or quantification of nucleic acid or protein." (Specification, page 21, lines 11-12.)

Further:

> A variety of protocols including ELISA, RIA, and FACS for measuring HTAP are known in the art and provide a basis for diagnosing altered or abnormal levels of HTAP expression. Normal or standard values for HTAP expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to HTAP under conditions suitable for complex formation. The amount of standard complex formation may be quantified by various methods, but preferably by photometric means. Quantities of HTAP expressed in subject, control and disease, samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease. (Specification, page 33, lines 8-16.)

Moreover, the Specification discloses that " HTAP, its catalytic or immunogenic fragments or oligopeptides thereof, can be used for screening libraries of compounds in any of a variety of drug screening techniques" and that "one may use competitive drug screening assays in which neutralizing antibodies capable of binding HTAP specifically compete with a test compound for binding HTAP." (Specification, page 37, lines 18-20 and page 38, lines 3-5.)

7. The Examiner's reliance on *Brenner* v. *Manson* is misplaced

This is not a case in which biological function or disease association or differential expression is necessary to provide a link between the claimed invention on one hand, and a compound of known utility on the other. Given that the claimed invention is disclosed in the parent Hillman '260 application to be useful as a tool in a number of gene and protein expression monitoring applications that were well-known at the time of the filing of the application in connection with the development of drugs and the monitoring of the activity of drugs, the precise biological function or disease association or differential expression of the claimed polypeptide is superfluous information for the purposes of establishing utility.

The fact that the claimed invention already has a disclosed use as a tool in then available technology (such as expression profiling using 2-D PAGE) distinguishes it from those few claimed inventions found not to have utility. In each of those cases, unlike this one, the person of ordinary skill in the art was left to guess whether the claimed invention could be used to produce an identifiable benefit. Thus the Examiner's unsupported statement that one of those cases, *Brenner* v. *Manson*, 383 U.S. 519, 532, 534-35 (1966), is somehow analogous to this case is plainly incorrect. (Final Office Action, page 9.)

Brenner concerns a narrow exception to the general rule that inventions are useful. It holds that where the assertion of utility for the claimed invention is made by association with a group including useful members, the group may not include so many useless members that there would be less than a substantial likelihood that the claimed invention is in fact one of the useful members of the group. In *Brenner*, the claimed invention was a process for making a synthetic steroid. Some steroids are useful, but most are not. While the claimed process in *Brenner* produced a composition that bore homology to some useful steroids, antitumor agents, it also bore structural homology to a substantial number of steroids having no utility at all. There was no evidence that could show, by substantial likelihood, that the claimed invention would produce the benefits of the small subset of useful steroids. It was entirely possible, and indeed likely, that the claimed invention was just as useless as the majority of steroids.

In *Brenner*, the steroid was not disclosed in the application for a patent to be useful in its then-present form. Here, in contrast, the claimed SEQ ID NO:1 polypeptide is an expressed polypeptide that was disclosed to be useful in the parent Hillman '260 application for many known applications involving gene and protein expression monitoring analysis. Its utility is not a matter of guesswork. It is not a random DNA or protein sequences that might or might not be useful as a scientific tool. Unlike the steroid in *Brenner*, the utility of the invention claimed here is not grounded upon being structurally analogous to a molecule which belongs to a class of molecules containing a significant number of useless compositions.

And, the utilities disclosed in the application are for purposes other than just studying the claimed invention itself, *Brenner*, 383 U.S. at 535, i.e., for other (non self-referential) uses such as to ascertain the toxic potential of a drug candidate and to study the efficacy of a proposed drug. Indeed, in view of the Furness Declaration (at, e.g., ¶ 12), the evidence shows that persons

skilled in the art on March 20, 1997, who read the Hillman '260 application, would have believed the claimed polypeptides to be so useful that they would request specifically that any 2-D PAGE map that was being used in connection with developing new drugs for the treatment of disorders associated with cell proliferation and inflammation utilize the SEQ ID NO:1 polypeptide sequence.

Accordingly, in this case, biological function or disease association or differential expression is in fact superfluous information for the purposes of demonstrating utility. Here, the claimed invention is more than "substantially likely" to be useful, in a way that is utterly independent of knowledge of precise biological function or disease association or differential expression, as the Furness Declaration and other evidence presented by the Appellants demonstrates. Given that the claimed invention has disclosed and well-established utilities, the Appellants need not demonstrate utility by imputation or by showing disease association or differential expression.

In the end, the Examiner has failed to recognize that new technologies, such as those involving the use of 2-D PAGE to conduct protein expression analyses, have made useful biological molecules that might not otherwise have been useful in the past. *See Brenner*, 383 U.S. at 536. Technology has now advanced well beyond the point that a person of ordinary skill in the art would have to guess whether a newly discovered expressed polypeptide could be usefully employed without further research. It has created a need for new tools, such as the claimed polypeptide, that provide, and have been providing for some time now, unquestioned commercial and scientific benefits, and **real-world benefits** to the public by enabling faster, cheaper and safer drug discovery processes. The Examiner is obliged, by law, to recognize this reality.

IV. By Requiring the Patent Applicant to Assert a Particular or Unique Utility, the Patent Examination Utility Guidelines and Training Materials Applied by the Patent Examiner Misstate the Law

There is an additional, independent reason to overturn the rejections: to the extent the rejections are based on Revised Interim Utility Examination Guidelines (64 FR 71427, December 21, 1999), the final Utility Examination Guidelines (66 FR 1092, January 5, 2001)

and/or the Revised Interim Utility Guidelines Training Materials (USPTO Website www.uspto.gov, March 1, 2000), the Guidelines and Training Materials are themselves inconsistent with the law.

The Training Materials, which direct the Examiners regarding how to apply the Utility Guidelines, address the issue of specificity with reference to two kinds of asserted utilities: "specific" utilities, which meet the statutory requirements, and "general" utilities, which do not. The Training Materials define a "specific utility" as follows:

> A [specific utility] is *specific* to the subject matter claimed. This contrasts to *general* utility that would be applicable to the broad class of invention. For example, a claim to a polynucleotide whose use is disclosed simply as "gene probe" or "chromosome marker" would not be considered to be specific in the absence of a disclosure of a specific DNA target. Similarly, a general statement of diagnostic utility, such as diagnosing an unspecified disease, would ordinarily be insufficient absent a disclosure of what condition can be diagnosed.

The Training Materials distinguish between "specific" and "general" utilities by assessing whether the asserted utility is sufficiently "particular," *i.e.*, unique (Training Materials at p.52) as compared to the "broad class of invention." (In this regard, the Training Materials appear to parallel the view set forth in Stephen G. Kunin, Written Description Guidelines and Utility Guidelines, 82 J.P.T.O.S. 77, 97 (Feb. 2000) ("With regard to the issue of specific utility the question to ask is whether or not a utility set forth in the specification is *particular* to the claimed invention.").)

Such "unique" or "particular" utilities never have been required by the law. To meet the utility requirement, the invention need only be "practically useful," *Natta*, 480 F.2d 1 at 1397, and confer a "specific benefit" on the public. *Brenner*, 383 U.S. at 534. Thus incredible "throwaway" utilities, such as trying to "patent a transgenic mouse by saying it makes great snake food," do not meet this standard. Karen Hall, Genomic Warfare, The American Lawyer 68 (June 2000) (quoting John Doll, Chief of the Biotech Section of USPTO).

This does not preclude, however, a general utility, contrary to the statement in the Training Materials where "specific utility" is defined (page 5). Practical real-world uses are not limited to uses that are unique to an invention. The law requires that the practical utility be "definite," not particular. *Montedison*, 664 F.2d at 375. Appellant is not aware of any court that has rejected an assertion of utility on the grounds that it is not "particular" or "unique" to the

specific invention. Where courts have found utility to be too "general," it has been in those cases in which the asserted utility in the patent disclosure was not a practical use that conferred a specific benefit. That is, a person of ordinary skill in the art would have been left to guess as to how to benefit at all from the invention. In *Kirk*, for example, the CCPA held the assertion that a man-made steroid had "useful biological activity" was insufficient where there was no information in the specification as to how that biological activity could be practically used. *Kirk*, 376 F.2d at 941.

The fact that an invention can have a particular use does not provide a basis for requiring a particular use. *See Brana*, *supra* (disclosure describing a claimed antitumor compound as being homologous to an antitumor compound having activity against a "particular" type of cancer was determined to satisfy the specificity requirement). "Particularity" is not and never has been the *sine qua non* of utility; it is, at most, one of many factors to be considered.

As described *supra*, broad classes of inventions can satisfy the utility requirement so long as a person of ordinary skill in the art would understand how to achieve a practical benefit from knowledge of the class. Only classes that encompass a significant portion of nonuseful members would fail to meet the utility requirement. *Supra* § III.B. (*Montedison,* 664 F.2d at 374-75).

The Training Materials fail to distinguish between broad classes that convey information of practical utility and those that do not, lumping all of them into the latter, unpatentable category of "general" utilities. As a result, the Training Materials paint with too broad a brush. Rigorously applied, they would render unpatentable whole categories of inventions heretofore considered to be patentable, and that have indisputably benefitted the public, including the claimed invention. *See supra* § III.B. Thus the Training Materials cannot be applied consistently with the law.

Issue 3Enablement Rejection

The rejection set forth in the Final Office Action is based on the assertions discussed above, i.e., that the claimed invention lacks patentable utility. To the extent that the rejection under § 112, first paragraph, is based on the improper allegation of lack of patentable utility under § 101, it fails for the same reasons.

(9) CONCLUSION

Appellants request that the rejections of the claims on appeal be reversed for at least the reasons above.

Appellants respectfully submit that rejections for lack of utility based, *inter alia*, on an allegation of "lack of specificity," as set forth in the Office Action and as justified in the Revised Interim and final Utility Guidelines and Training Materials, are not supported in the law. Neither are they scientifically correct, nor supported by any evidence or sound scientific reasoning. These rejections are alleged to be founded on facts in court cases such as *Brenner* and *Kirk*, yet those facts are clearly distinguishable from the facts of the instant application, and indeed most if not all nucleotide and protein sequence applications. Nevertheless, the PTO is attempting to mold the facts and holdings of these prior cases, "like a nose of wax,"[6] to target rejections of claims to polypeptides and polynucleotides where biological activity information has not been proven by laboratory experimentation, and they have done so by ignoring perfectly acceptable utilities fully disclosed in the specifications as well as well-established utilities known to those of skill in the art. As is disclosed in the specification, and even more clearly, as one of ordinary skill in the art would understand, the claimed invention has well-established, specific, substantial and credible utilities. The rejections are, therefore, improper and should be reversed.

Moreover, to the extent the above rejections were based on the Revised Interim and final Examination Guidelines and Training Materials, those portions of the Guidelines and Training Materials that form the basis for the rejections should be determined to be inconsistent with the law.

Due to the urgency of this matter and its economic and public health implications, an expedited review of this appeal is earnestly solicited.

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[6]"The concept of patentable subject matter under §101 is not 'like a nose of wax which may be turned and twisted in any direction * * *.' *White v. Dunbar*, 119 U.S. 47, 51." *(Parker v. Flook,* 198 USPQ 193 (US SupCt 1978))

If the USPTO determines that any additional fees are due, the Commissioner is hereby authorized to charge Deposit Account No. **09-0108.**

This brief is enclosed in triplicate.

Respectfully submitted,

INCYTE CORPORATION

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Enclosures:

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2. H. Hegyi and M. Gerstein, Annotation Transfer for Genomics: Measuring Functional Divergence in Multi-Domain Proteins, Genome Research 11: 1632-1640 (2001)
3. J. C. Rockett, et. al., Differential gene expression in drug metabolism and toxicology: practicalities, problems, and potential, Xenobiotica 29:655-691 (1999)
4. E. F. Nuwaysir, et al., Microarrays and Toxicology: The Advent of Toxicogenomics, Molecular Carcinogenesis 24:153-159 (1999)
5. S. Steiner and N. L. Anderson, Expression profiling in toxicology -- potentials and limitations, Toxicology Letters 112-13:467-471 (2000)
6. Email from the primary investigator, Dr. Cynthia Afshari to an Incyte employee, dated July 3, 2000, as well as the original message to which she was responding
7. J.E. Celis et al., Human Cellular Protein Patterns and their Link to Genome DNA Sequence Data: Usefulness of Two-Dimensional Gel Electrophoresis and Microsequencing, FASEB Journal, 5, 2200-2208 (1991)

APPENDIX - CLAIMS ON APPEAL

1. (As Once Amended) An isolated polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence of SEQ ID NO:1,

b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1, and

c) an immunogenic fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1.

2. (As Once Amended) An isolated polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

15. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

16. (As Once Amended) A composition of claim 15, wherein the polypeptide comprises an amino acid sequence of SEQ ID NO:1.